SEQUENCE LISTING

<110> McCarthy, Sean A.

<120> NOVEL CRSP PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREFOR

<130> MEI-008

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<150> 08/842,898
<151> 1997-04-17

<150> 60/071,589
<151> 1998-01-15

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<170> PatentIn Ver. 2.0

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Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala Val Pro Thr Ala Pro Ala
10 15 20

ccc gct ccg acg gcg acc tcg gct cca gtc aag ccc ggc ccg gct ctc 151
Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu
25 30 35

agc tac ccg cag gag gag gcc acc ctc aat gag atg ttc cgc gag gtt 199
Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val
40 45 50

gag gaa ctg atg gag gac acg cag cac aaa ttg cgc agc gcg gtg gaa 247
Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu
55 60 65 70

gag atg gag gca gaa gaa gct gct gct aaa gca tca tca gaa gtg aac 295
Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Ala Ser Ser Glu Val Asn
75 80 85

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ctg gca aac tta cct ccc agc tat cac aat gag acc aac aca gac acg   343
Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr
            90                  95                  100

aac gtt gga aat aat acc atc cat gtg cac cga gaa att cac aag ata   391
Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile
        105                 110                 115

acc aac aac cag act gga caa atg gtc ttt tca gag aca gtt atc aca   439
Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr
    120                 125                 130

tct gtg gga gac gaa gaa ggc aga agg agc cac gag tgc atc atc gac   487
Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp
135                 140                 145                 150

gag gac tgt ggg ccc agc atg tac tgc cag ttt gcc agc ttc cag tac   535
Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr
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acc tgc cag cca tgc cgg ggc cag agg atg ctc tgc acc cgg gac agt   583
Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser
            170                 175                 180

gag tgc tgt gga gac cag ctg tgt gtc tgg ggt cac tgc acc aaa atg   631
Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met
        185                 190                 195

gcc acc agg ggc agc aat ggg acc atc tgt gac aac cag agg gac tgc   679
Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys
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cag ccg ggg ctg tgc tgt gcc ttc cag aga ggc ctg ctg ttc cct gtg   727
Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val
215                 220                 225                 230

tgc aca ccc ctg ccc gtg gag ggc gag ctt tgc cat gac ccc gcc agc   775
Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser
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cgg ctt ctg gac ctc atc acc tgg gag cta gag cct gat gga gcc ttg   823
Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu
            250                 255                 260

gac cga tgc cct tgt gcc agt ggc ctc ctc tgc cag ccc cac agc cac   871
Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His
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agc ctg gtg tat gtg tgc aag ccg acc ttc gtg ggg agc cgt gac caa   919
Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln
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gat ggg gag atc ctg ctg ccc aga gag gtc ccc gat gag tat gaa gtt   967
Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val
295                 300                 305                 310
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ggc agc ttc atg gag gag gtg cgc cag gag ctg gag gac ctg gag agg 1015
Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg
315 320 325

agc ctg act gaa gag atg gcg ctg agg gag cct gcg gct gcc gcc gct 1063
Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala Ala
330 335 340

gca ctg ctg gga agg gaa gag att tagatctgga ccaggctgtg ggtagatgtg 1117
Ala Leu Leu Gly Arg Glu Glu Ile
345 350

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ggcgaggatt ataaatgaaa tttgcaaaat cacttagcag caactgaaga caattatcaa 2197

ccacgtggag aaaatcaaac cgagcagggc tgtgtgaaac atggttgtaa tatgcgactg 2257

cgaacactga actctacgcc actccacaaa tgatgttttc aggtgtcatg gactgttgcc 2317

accatgtatt catccagagt tcttaaagtt taaagttgca catgattgta taagcatgct 2377

ttctttgagt tttaaattat gtataaacat aagttgcatt tagaaatcaa gcataaatca 2437

cttcaactgc taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2479

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<213> Homo sapiens

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             20                  25                  30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
         35                  40                  45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
     50                  55                  60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
 65                  70                  75                  80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
                 85                  90                  95

Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
            100                 105                 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
        115                 120                 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
    130                 135                 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145                 150                 155                 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
                165                 170                 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
            180                 185                 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
        195                 200                 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
    210                 215                 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225                 230                 235                 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
                245                 250                 255
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Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
            260                 265                 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
        275                 280                 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
    290                 295                 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
305                 310                 315                 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
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Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Arg Glu Glu Ile
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  1               5                  10                  15

gtc ccc acg gcc ccc gcg ccc gct ccg acg gcg acc tcg gct cca gtc   96
Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
             20                  25                  30

aag ccc ggc ccg gct ctc agc tac ccg cag gag gag gcc acc ctc aat  144
Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
         35                  40                  45

gag atg ttc cgc gag gtt gag gaa ctg atg gag gac acg cag cac aaa  192
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
     50                  55                  60

ttg cgc agc gcg gtg gaa gag atg gag gca gaa gaa gct gct gct aaa  240
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
 65                  70                  75                  80

gca tca tca gaa gtg aac ctg gca aac tta cct ccc agc tat cac aat  288
Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
                 85                  90                  95

gag acc aac aca gac acg aac gtt gga aat aat acc atc cat gtg cac  336
Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
            100                 105                 110
```

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cga gaa att cac aag ata acc aac aac cag act gga caa atg gtc ttt   384
Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
        115                 120                 125

tca gag aca gtt atc aca tct gtg gga gac gaa gaa ggc aga agg agc   432
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
    130                 135                 140

cac gag tgc atc atc gac gag gac tgt ggg ccc agc atg tac tgc cag   480
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145                 150                 155                 160

ttt gcc agc ttc cag tac acc tgc cag cca tgc cgg ggc cag agg atg   528
Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
                165                 170                 175

ctc tgc acc cgg gac agt gag tgc tgt gga gac cag ctg tgt gtc tgg   576
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
            180                 185                 190

ggt cac tgc acc aaa atg gcc acc agg ggc agc aat ggg acc atc tgt   624
Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
        195                 200                 205

gac aac cag agg gac tgc cag ccg ggg ctg tgc tgt gcc ttc cag aga   672
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
    210                 215°                220

ggc ctg ctg ttc cct gtg tgc aca ccc ctg ccc gtg gag ggc gag ctt   720
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225                 230                 235                 240

tgc cat gac ccc gcc agc cgg ctt ctg gac ctc atc acc tgg gag cta   768
Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
                245                 250                 255

gag cct gat gga gcc ttg gac cga tgc cct tgt gcc agt ggc ctc ctc   816
Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
            260                 265                 270

tgc cag ccc cac agc cac agc ctg gtg tat gtg tgc aag ccg acc ttc   864
Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
        275                 280                 285

gtg ggg agc cgt gac caa gat ggg gag atc ctg ctg ccc aga gag gtc   912
Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
    290                 295                 300

ccc gat gag tat gaa gtt ggc agc ttc atg gag gag gtg cgc cag gag   960
Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
305                 310                 315                 320

ctg gag gac ctg gag agg agc ctg act gaa gag atg gcg ctg agg gag  1008
Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
                325                 330                 335
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aagg atg gtg gcg gcc gtc ctg ctg ggg ctg agc tgg ctc tgc tct ccc  169
     Met Val Ala Ala Val Leu Leu Gly Leu Ser Trp Leu Cys Ser Pro
       1               5                  10                  15

ctg gga gct ctg gtc ctg gac ttc aac aac atc agg agc tct gct gac  217
Leu Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp
                20                  25                  30

ctg cat ggg gcc cgg aag ggc tca cag tgc ctg tct gac acg gac tgc  265
Leu His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys
            35                  40                  45

aat acc aga aag ttc tgc ctc cag ccc cgc gat gag aag ccg ttc tgt  313
Asn Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys
        50                  55                  60

gct aca tgt cgt ggg ttg cgg agg agg tgc cag cga gat gcc atg tgc  361
Ala Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys
    65                  70                  75

tgc cct ggg aca ctc tgt gtg aac gat gtt tgt act acg atg gaa gat  409
Cys Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp
80                  85                  90                  95

gca acc cca ata tta gaa agg cag ctt gat gag caa gat ggc aca cat  457
Ala Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His
                100                 105                 110

gca gaa gga aca act ggg cac cca gtc cag gaa aac caa ccc aaa agg  505
Ala Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg
            115                 120                 125

aag cca agt att aag aaa tca caa ggc agg aag gga caa gag gga gaa  553
Lys Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu
        130                 135                 140
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agt tgt ctg aga act ttt gac tgt ggc cct gga ctt tgc tgt gct cgt   601
Ser Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg
    145                 150                 155

cat ttt tgg acg aaa att tgt aag cca gtc ctt ttg gag gga cag gtc   649
His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val
160                 165                 170                 175

tgc tcc aga aga ggg cat aaa gac act gct caa gct cca gaa atc ttc   697
Cys Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe
                180                 185                 190

cag cgt tgc gac tgt ggc cct gga cta ctg tgt cga agc caa ttg acc   745
Gln Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr
            195                 200                 205

agc aat cgg cag cat gct cga tta aga gta tgc caa aaa ata gaa aag   793
Ser Asn Arg Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys
        210                 215                 220

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Leu
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             20                  25                  30

His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn
         35                  40                  45

Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala
     50                  55                  60

Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys Cys
 65                  70                  75                  80

Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala
                 85                  90                  95

Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala
            100                 105                 110

Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys
        115                 120                 125

Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser
    130                 135                 140
```

```
Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
145                 150                 155                 160

Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys
                165                 170                 175

Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln
            180                 185                 190

Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr Ser
        195                 200                 205

Asn Arg Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys Leu
    210                 215                 220


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  1               5                  10                  15

gga gct ctg gtc ctg gac ttc aac aac atc agg agc tct gct gac ctg   96
Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp Leu
             20                  25                  30

cat ggg gcc cgg aag ggc tca cag tgc ctg tct gac acg gac tgc aat   144
His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn
         35                  40                  45

acc aga aag ttc tgc ctc cag ccc cgc gat gag aag ccg ttc tgt gct   192
Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala
     50                  55                  60

aca tgt cgt ggg ttg cgg agg agg tgc cag cga gat gcc atg tgc tgc   240
Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys Cys
 65                  70                  75                  80

cct ggg aca ctc tgt gtg aac gat gtt tgt act acg atg gaa gat gca   288
Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala
                 85                  90                  95

acc cca ata tta gaa agg cag ctt gat gag caa gat ggc aca cat gca   336
Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala
            100                 105                 110

gaa gga aca act ggg cac cca gtc cag gaa aac caa ccc aaa agg aag   384
Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys
        115                 120                 125
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cca agt att aag aaa tca caa ggc agg aag gga caa gag gga gaa agt   432
Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser
    130                 135                 140

tgt ctg aga act ttt gac tgt ggc cct gga ctt tgc tgt gct cgt cat   480
Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
145                 150                 155                 160

ttt tgg acg aaa att tgt aag cca gtc ctt ttg gag gga cag gtc tgc   528
Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys
                165                 170                 175

tcc aga aga ggg cat aaa gac act gct caa gct cca gaa atc ttc cag   576
Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln
            180                 185                 190

cgt tgc gac tgt ggc cct gga cta ctg tgt cga agc caa ttg acc agc   624
Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr Ser
        195                 200                 205

aat cgg cag cat gct cga tta aga gta tgc caa aaa ata gaa aag cta   672
Asn Arg Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys Leu
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ctctttcttt ctccctcttg agtccttctg ag atg atg gct ctg ggc gca gcg   113
                                    Met Met Ala Leu Gly Ala Ala
                                      1               5

gga gct acc cgg gtc ttt gtc gcg atg gta gcg gcg gct ctc ggc ggc   161
Gly Ala Thr Arg Val Phe Val Ala Met Val Ala Ala Ala Leu Gly Gly
         10                  15                  20

cac cct ctg ctg gga gtg agc gcc acc ttg aac tcg gtt ctc aat tcc   209
His Pro Leu Leu Gly Val Ser Ala Thr Leu Asn Ser Val Leu Asn Ser
     25                  30                  35

aac gct atc aag aac ctg ccc cca ccg ctg ggc ggc gct gcg ggg cac   257
Asn Ala Ile Lys Asn Leu Pro Pro Pro Leu Gly Gly Ala Ala Gly His
 40                  45                  50                  55

cca ggc tct gca gtc agc gcc gcg ccg gga atc ctg tac ccg ggc ggg   305
Pro Gly Ser Ala Val Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly
                 60                  65                  70
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aat aag tac cag acc att gac aac tac cag ccg tac ccg tgc gca gag   353
Asn Lys Tyr Gln Thr Ile Asp Asn Tyr Gln Pro Tyr Pro Cys Ala Glu
            75                  80                  85

gac gag gag tgc ggc act gat gag tac tgc gct agt ccc acc cgc gga   401
Asp Glu Glu Cys Gly Thr Asp Glu Tyr Cys Ala Ser Pro Thr Arg Gly
        90                  95                  100

ggg gac gca ggc gtg caa atc tgt ctc gcc tgc agg aag cgc cga aaa   449
Gly Asp Ala Gly Val Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys
    105                 110                 115

cgc tgc atg cgt cac gct atg tgc tgc ccc ggg aat tac tgc aaa aat   497
Arg Cys Met Arg His Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn
120                 125                 130                 135

gga ata tgc gtg tct tct gat caa aat cat ttc cga gga gaa att gag   545
Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg Gly Glu Ile Glu
                140                 145                 150

gaa acc atc act gaa agc ttt ggt aat gat cat agc acc ttg gat ggg   593
Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser Thr Leu Asp Gly
            155                 160                 165

tat tcc aga aga acc acc ttg tct tca aaa atg tat cac acc aaa gga   641
Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr His Thr Lys Gly
        170                 175                 180

caa gaa ggt tct gtt tgt ctc cgg tca tca gac tgt gcc tca gga ttg   689
Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys Ala Ser Gly Leu
    185                 190                 195

tgt tgt gct aga cac ttc tgg tcc aag atc tgt aaa cct gtc ctg aaa   737
Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys Lys Pro Val Leu Lys
200                 205                 210                 215

gaa ggt caa gtg tgt acc aag cat agg aga aaa ggc tct cat gga cta   785
Glu Gly Gln Val Cys Thr Lys His Arg Arg Lys Gly Ser His Gly Leu
                220                 225                 230

gaa ata ttc cag cgt tgt tac tgt gga gaa ggt ctg tct tgc cgg ata   833
Glu Ile Phe Gln Arg Cys Tyr Cys Gly Glu Gly Leu Ser Cys Arg Ile
            235                 240                 245

cag aaa gat cac cat caa gcc agt aat tct tct agg ctt cac act tgt   881
Gln Lys Asp His His Gln Ala Ser Asn Ser Ser Arg Leu His Thr Cys
        250                 255                 260

cag aga cac taaaccagct atccaaaatg cagtgaactc cttttatata           930
Gln Arg His
    265

atagatgcta tgaaaacctt ttatgacctt catcaactca atcctaagga tatacaagtt 990

ctgtggtttc agttaagcat tccaataaca ccttccaaaa acctggagtg taagagcttt 1050
```

gtttctttat ggaactcccc tgtgattgca gtaaattact gtattgtaaa ttctcagtgt 1110

ggcacttacc tgtaaatgca atgaaacttt taattatttt tctaaaggtg ctgcactgcc 1170

tatttttcct cttgttatgt aaatttttgt acacattgat tgttatcttg actgacaaat 1230

attctatatt gaactgaagt aaatcatttc agcttatagt tcttaaaagc ataacccttt 1290

accccatttn attctagagt cnagaacgca aggatctctt ggaatgacaa atgataggta 1350

cctaaaatgt aacatgaaaa tactagctta ttttctgaaa tgtactatct taatgcttaa 1410

attatatttc cctttaggct gtgatagttt ttgaaataaa atttaacatt taatatcatg 1470

aaatgktata agtagacata aaaaaaaaaa aaaaaaaaaa agggcggccg ctagactag 1529

<210> 8
<211> 266
<212> PRT
<213> Homo sapiens

<400> 8

```
Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met
  1               5                  10                  15

Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr
             20                  25                  30

Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro
         35                  40                  45

Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro
     50                  55                  60

Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr
 65                  70                  75                  80

Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr
                 85                  90                  95

Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu
            100                 105                 110

Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys
        115                 120                 125

Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn
    130                 135                 140

His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn
145                 150                 155                 160

Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser
                165                 170                 175
```

```
Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser
            180                 185                 190

Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys
        195                 200                 205

Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg
    210                 215                 220

Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly
225                 230                 235                 240

Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn
                245                 250                 255

Ser Ser Arg Leu His Thr Cys Gln Arg His
            260                 265
```

<210> 9
<211> 798
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(798)

<400> 9

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atg atg gct ctg ggc gca gcg gga gct acc cgg gtc ttt gtc gcg atg   48
Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met
  1               5                  10                  15

gta gcg gcg gct ctc ggc ggc cac cct ctg ctg gga gtg agc gcc acc   96
Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr
            20                  25                  30

ttg aac tcg gtt ctc aat tcc aac gct atc aag aac ctg ccc cca ccg   144
Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro
        35                  40                  45

ctg ggc ggc gct gcg ggg cac cca ggc tct gca gtc agc gcc gcg ccg   192
Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro
    50                  55                  60

gga atc ctg tac ccg ggc ggg aat aag tac cag acc att gac aac tac   240
Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr
65                  70                  75                  80

cag ccg tac ccg tgc gca gag gac gag gag tgc ggc act gat gag tac   288
Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr
                85                  90                  95

tgc gct agt ccc acc cgc gga ggg gac gca ggc gtg caa atc tgt ctc   336
Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu
            100                 105                 110
```

```
gcc tgc agg aag cgc cga aaa cgc tgc atg cgt cac gct atg tgc tgc   384
Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys
        115                 120                 125

ccc ggg aat tac tgc aaa aat gga ata tgc gtg tct tct gat caa aat   432
Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn
    130                 135                 140

cat ttc cga gga gaa att gag gaa acc atc act gaa agc ttt ggt aat   480
His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn
145                 150                 155                 160

gat cat agc acc ttg gat ggg tat tcc aga aga acc acc ttg tct tca   528
Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser
                165                 170                 175

aaa atg tat cac acc aaa gga caa gaa ggt tct gtt tgt ctc cgg tca   576
Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser
            180                 185                 190

tca gac tgt gcc tca gga ttg tgt tgt gct aga cac ttc tgg tcc aag   624
Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys
        195                 200                 205

atc tgt aaa cct gtc ctg aaa gaa ggt caa gtg tgt acc aag cat agg   672
Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg
    210                 215                 220

aga aaa ggc tct cat gga cta gaa ata ttc cag cgt tgt tac tgt gga   720
Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly
225                 230                 235                 240

gaa ggt ctg tct tgc cgg ata cag aaa gat cac cat caa gcc agt aat   768
Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn
                245                 250                 255

tct tct agg ctt cac act tgt cag aga cac                          798
Ser Ser Arg Leu His Thr Cys Gln Arg His
            260                 265
```

<210> 10
<211> 702
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(537)

<400> 10

```
gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga   48
Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
 1               5                  10                  15
```

```
tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga   96
Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
             20                  25                  30

gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc   144
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
         35                  40                  45

cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt   192
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
     50                  55                  60

act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg   240
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
 65                  70                  75                  80

gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa   288
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
                 85                  90                  95

ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg   336
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
            100                 105                 110

ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc   384
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
        115                 120                 125

cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg   432
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
    130                 135                 140

ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa   480
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
145                 150                 155                 160

gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt   528
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
                165                 170                 175

cag aaa att tgatcaccat tgaggaacat catcaattgc agactgtgaa           577
Gln Lys Ile

gttgtgtatt taatgcatta tagcatggtg gaaaataagg ttcagatgca gaagaatggc 637

taaaataaga aacgtgataa gaatatagat gatcacaaaa aaaaaaaaaa aaaagatgcg 697

gccgc                                                             702


<210> 11
<211> 179
<212> PRT
<213> Homo sapiens

<400> 11
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Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
 1               5                  10                  15

Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
            20                  25                  30

Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
        35                  40                  45

Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
    50                  55                  60

Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
65                  70                  75                  80

Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
                85                  90                  95

Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
            100                 105                 110

Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
        115                 120                 125

His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
    130                 135                 140

Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
145                 150                 155                 160

Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
                165                 170                 175

Gln Lys Ile
```

<210> 12
<211> 537
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(537)

<400> 12

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gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga   48
Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
 1               5                  10                  15

tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga   96
Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
            20                  25                  30
```

```
gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc   144
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
         35                  40                  45

cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt   192
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
     50                  55                  60

act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg   240
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
 65                  70                  75                  80

gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa   288
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
                 85                  90                  95

ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg   336
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
            100                 105                 110

ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc   384
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
        115                 120                 125

cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg   432
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
    130                 135                 140

ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa   480
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
145                 150                 155                 160

gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt   528
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
                165                 170                 175

cag aaa att                                                      537
Gln Lys Ile
```

<210> 13
<211> 928
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (75)..(800)

<400> 13

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ctcgaggcca aaattcggca cgaggccggg ctgtggtcta gcataaaggc ggagcccaga 60

agaaggggcg gggt atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg   110
              Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg
                1               5                  10
```

```
cat ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc   158
His Leu Leu Val Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser
         15                  20                  25

gct gca gct cct atc cat gat gct gac gcc caa gag agc tcc ttg ggt   206
Ala Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly
     30                  35                  40

ctc aca ggc ctc cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg   254
Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu
 45                  50                  55                  60

aaa ggt aac ctg ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg   302
Lys Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met
                 65                  70                  75

gac ttc cgg ggc ctc cct ggg aac tac cac aaa gag gag aac cag gag   350
Asp Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu
             80                  85                  90

cac cag ctg ggg aac aac acc ctc tcc agc cac ctc cag atc gac aag   398
His Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys
         95                 100                 105

atg acc gac aac aag aca gga gag gtg ctg atc tcc gag aat gtg gtg   446
Met Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val
    110                 115                 120

gca tcc att caa cca gcg gag ggg agc ttc gag ggt gat ttg aag gta   494
Ala Ser Ile Gln Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val
125                 130                 135                 140

ccc agg atg gag gag aag gag gcc ctg gta ccc atc cag aag gcc acg   542
Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr
                145                 150                 155

gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att   590
Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile
            160                 165                 170

aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac   638
Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His
        175                 180                 185

tgg ctc agc gag aag cga cac cgc ctg cag gcc atc cgg gat gga ctc   686
Trp Leu Ser Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu
    190                 195                 200

cgc aag ggg acc cac aag gac gtc cta gaa gag ggg acc gag agc tcc   734
Arg Lys Gly Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser
205                 210                 215                 220

tcc cac tcc agg ctg tcc ccc cga aag acc cac tta ctg tac atc ctc   782
Ser His Ser Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu
                225                 230                 235
```

agg ccc tct cgg cag ctg taggggtggg gaccggggag cacctgcctg 830
Arg Pro Ser Arg Gln Leu
240

tagcccccat cagaccctgc cccaagcacc atatggaaat aaagttcttt cttacatcta 890

aaaaaaaaaa aaaaaaaaaa aaaaaaattg gcggccgc 928

<210> 14
<211> 242
<212> PRT
<213> Homo sapiens

<400> 14
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
1 5 10 15

Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
20 25 30

Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
35 40 45

Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
50 55 60

Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
65 70 75 80

Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
85 90 95

Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
100 105 110

Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
115 120 125

Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
130 135 140

Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His
145 150 155 160

Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
165 170 175

Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu
180 185 190

Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
195 200 205

His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg
210 215 220

```
Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg
225                 230                 235                 240

Gln Leu
```

<210> 15
<211> 726
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(726)

<400> 15

```
atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg cat ctg ctg gtc   48
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
  1               5                  10                  15

ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc gct gca gct cct   96
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
            20                  25                  30

atc cat gat gct gac gcc caa gag agc tcc ttg ggt ctc aca ggc ctc   144
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
        35                  40                  45

cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg aaa ggt aac ctg   192
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
    50                  55                  60

ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg gac ttc cgg ggc   240
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
65                  70                  75                  80

ctc cct ggg aac tac cac aaa gag gag aac cag gag cac cag ctg ggg   288
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
                85                  90                  95

aac aac acc ctc tcc agc cac ctc cag atc gac aag atg acc gac aac   336
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
            100                 105                 110

aag aca gga gag gtg ctg atc tcc gag aat gtg gtg gca tcc att caa   384
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
        115                 120                 125

cca gcg gag ggg agc ttc gag ggt gat ttg aag gta ccc agg atg gag   432
Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
    130                 135                 140

gag aag gag gcc ctg gta ccc atc cag aag gcc acg gac agc ttc cac   480
Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His
145                 150                 155                 160
```

```
aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att aag ctg cca cgg   528
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
                165                 170                 175

cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac tgg ctc agc gag   576
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu
            180                 185                 190

aag cga cac cgc ctg cag gcc atc cgg gat gga ctc cgc aag ggg acc   624
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
        195                 200                 205

cac aag gac gtc cta gaa gag ggg acc gag agc tcc tcc cac tcc agg   672
His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg
    210                 215                 220

ctg tcc ccc cga aag acc cac tta ctg tac atc ctc agg ccc tct cgg   720
Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg
225                 230                 235                 240

cag ctg                                                           726
Gln Leu


<210> 16
<211> 2381
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (110)..(1156)

<400> 16
mgtcgaccca cgcgtccgct gtggcagccc agctaccggt cgtgaccaga tccagcttgc 60

agctcagctt tgttcattcg aattgggcgg cggccagcgc ggaacaaac atg cag cgg 118
                                                    Met Gln Arg
                                                      1

ctc ggg ggt att ttg ctg tgt aca ctg ctg gcg gcg gcg gtc ccc act   166
Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala Val Pro Thr
      5                  10                  15

gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg gag ccg ggc   214
Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala Glu Pro Gly
 20                  25                  30                  35

cca gct ctc aac tac cct cag gag gaa gct acg ctc aat gag atg ttt   262
Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe
                40                  45                  50

cga gag gtg gag gag ctg atg gaa gac act cag cac aaa ctg cgc agt   310
Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser
            55                  60                  65
```

```
gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa acg tcc tct   358
Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Thr Ser Ser
         70                  75                  80

gag gtg aac ctg gca agc tta cct ccc aac tat cac aat gag acc agc   406
Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn Glu Thr Ser
     85                  90                  95

acg gag acc agg gtg gga aat aac aca gtc cat gtg cac cag gaa gtt   454
Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His Gln Glu Val
100                 105                 110                 115

cac aag ata acc aac aac cag agt gga cag gtg gtc ttt tct gag aca   502
His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe Ser Glu Thr
                120                 125                 130

gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc cat gaa tgt   550
Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser His Glu Cys
            135                 140                 145

atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag ttc tcc agc   598
Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln Phe Ser Ser
        150                 155                 160

ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg cta tgc acc   646
Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met Leu Cys Thr
    165                 170                 175

cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg ggt cac tgc   694
Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp Gly His Cys
180                 185                 190                 195

acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt gac aac cag   742
Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys Asp Asn Gln
                200                 205                 210

agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga ggc ctg ctg   790
Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu
            215                 220                 225

ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc tgc cat gac   838
Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp
        230                 235                 240

ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg gag cct gaa   886
Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Glu
    245                 250                 255

gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta tgc cag cca   934
Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro
260                 265                 270                 275

cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc gtg ggc agc   982
His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe Val Gly Ser
                280                 285                 290
```

```
cat gac cac agt gag gag agc cag ctg ccc agg gag gcc ccg gat gag   1030
His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala Pro Asp Glu
            295                 300                 305

tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag ctg gaa gac   1078
Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu Leu Glu Asp
        310                 315                 320

ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg cct gcc cct   1126
Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly Pro Ala Pro
    325                 330                 335

gtg gag tca cta ggc gga gag gag gag att taggcccaga cccagctgag     1176
Val Glu Ser Leu Gly Gly Glu Glu Glu Ile
340                 345

tcactggtag atgtgcaata gaaatggcta atttattttc ccaggagtgt ccccaagtgt 1236

ggaatggccg cagctccttc ccagtagctt ttcctctggc ttgacaaggt acagtgcagt 1296

acatttcttc cagccgccct gcttctctga cttgggaaag acaggcatgg cgggtaaggg 1356

cagcggtgag tcgtccctcg ctgttgctag aaacgctgtc ttgttcttca tggatggaag 1416

atttgtttga agggagagga tgggaagggg tgaagtctgc tcatgatgga tttgggggat 1476

acagggagga ggatgcctgc cttgcagacg tggacttggc aaaatgtaac ctttgctttt 1536

gtcttgcgcc gctcccatgg gctgaggcag tggctacaca agagctatgc tgctctgtgg 1596

cctcccacat attcatccct gtgtttcagc tcctacctca ctgtcagcac agcccttcat 1656

agccacgccc cctcttgctc accacagcct aggaggggac cagaggggac ttctctcaga 1716

gccccatgct ctctctctca accccatacc agcctctgtg ccagcgacag tccttccaaa 1776

tggagggagt gaaatccttt ggtttaatta ttttctcctt caaggcacgc ctgccactaa 1836

ggtcaggctg acttgcatgt ccctctaacg ttcgtagcag tgtggtggac actgtcttcc 1896

accgactgct tcaatacctc tgaaagccag tgctcggagt gcagttcgtg taaattaatt 1956

tgcaggaagt atacttggct aattgtaggg ctaggattgt gaatgaaatt tgcaaagtcg 2016

cttagcaaca atggaaagcc tttctcagtc acaccgagaa gtcacaacca agccaggttg 2076

tgtagagtac agctgtgaca tacagacaga agaaggctgg gctggatgtc aggcctcaga 2136

tgacggtttc aggtgccagg aactattacc attctgtatc tatccagagt tattaaaatt 2196

gaaagttgca cacatttgta taagcatgcc tttctcctga gttttaaatt atatgtatac 2256

acaaacatgt ggccctcaaa gatcatgcac aaaccactac tctttgctaa ttcttggact 2316

tttctctttg attttcaata aatacaaatc cccttcatgc aaaaaaaaaa aaaaagggcg 2376

gccgc                                                             2381
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<210> 17
<211> 349
<212> PRT
<213> Homo sapiens

<400> 17

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Met Gln Arg Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala
 1               5                  10                  15

Val Pro Thr Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala
            20                  25                  30

Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
        35                  40                  45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
    50                  55                  60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65                  70                  75                  80

Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
                85                  90                  95

Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His
            100                 105                 110

Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe
        115                 120                 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser
    130                 135                 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln
145                 150                 155                 160

Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met
                165                 170                 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp
            180                 185                 190

Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys
        195                 200                 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
    210                 215                 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225                 230                 235                 240

Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu
                245                 250                 255
```

```
Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
            260                 265                 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe
        275                 280                 285

Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala
    290                 295                 300

Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu
305                 310                 315                 320

Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly
                325                 330                 335

Pro Ala Pro Val Glu Ser Leu Gly Gly Glu Glu Glu Ile
            340                 345
```

<210> 18
<211> 1047
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1047)

<400> 18

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atg cag cgg ctc ggg ggt att ttg ctg tgt aca ctg ctg gcg gcg gcg   48
Met Gln Arg Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala
  1               5                  10                  15

gtc ccc act gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg   96
Val Pro Thr Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala
            20                  25                  30

gag ccg ggc cca gct ctc aac tac cct cag gag gaa gct acg ctc aat  144
Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
        35                  40                  45

gag atg ttt cga gag gtg gag gag ctg atg gaa gac act cag cac aaa  192
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
    50                  55                  60

ctg cgc agt gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa  240
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65                  70                  75                  80

acg tcc tct gag gtg aac ctg gca agc tta cct ccc aac tat cac aat  288
Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
                85                  90                  95

gag acc agc acg gag acc agg gtg gga aat aac aca gtc cat gtg cac  336
Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His
            100                 105                 110
```

```
cag gaa gtt cac aag ata acc aac aac cag agt gga cag gtg gtc ttt   384
Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe
        115                 120                 125

tct gag aca gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc   432
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser
    130                 135                 140

cat gaa tgt atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag   480
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln
145                 150                 155                 160

ttc tcc agc ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg   528
Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met
                165                 170                 175

cta tgc acc cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg   576
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp
            180                 185                 190

ggt cac tgc acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt   624
Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys
        195                 200                 205

gac aac cag agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga   672
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
    210                 215                 220

ggc ctg ctg ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc   720
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225                 230                 235                 240

tgc cat gac ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg   768
Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu
                245                 250                 255

gag cct gaa gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta   816
Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
            260                 265                 270

tgc cag cca cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc   864
Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe
        275                 280                 285

gtg ggc agc cat gac cac agt gag gag agc cag ctg ccc agg gag gcc   912
Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala
    290                 295                 300

ccg gat gag tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag   960
Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu
305                 310                 315                 320

ctg gaa gac ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg   1008
Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly
                325                 330                 335
```

cct gcc cct gtg gag tca cta ggc gga gag gag gag att
Pro Ala Pro Val Glu Ser Leu Gly Gly Glu Glu Glu Ile 1047
340 345

<210> 19
<211> 8
<212> PRT
<213> synthtic construct

<400> 19
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5